

SEQUENCE LISTING

<110> Mahajan, Pramod B.

<120> Rad2/FEN-1 Orthologues and Uses
Thereof

<130> 0961D

<150> 09/426,557

<151> 1999-10-22

<150> 60/112,332

<151> 1998-12-15

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<170> FastSEQ for Windows Version 3.0

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<213> Zea mays

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                1               5

ctg gcg gac aat gcg ccc aag gcg atg aag gag cag aag ttc gag agc      159
Leu Ala Asp Asn Ala Pro Lys Ala Met Lys Glu Gln Lys Phe Glu Ser
10                15                20                25

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Tyr Phe Gly Arg Lys Ile Ala Val Asp Ala Ser Met Ser Ile Tyr Gln
30                35                40

ttc ctg att gta gtt gga agg aca ggc atg gaa act ctc aca aat gaa      255
Phe Leu Ile Val Val Gly Arg Thr Gly Met Glu Thr Leu Thr Asn Glu
45                50                55

gct ggt gaa gtc act agt cat ttg caa gga atg ttc aac cgg aca ata      303
Ala Gly Glu Val Thr Ser His Leu Gln Gly Met Phe Asn Arg Thr Ile
60                65                70

aga tta ctg gaa gcg gga atc aag cca gtt tat gtt ttt gat ggc aag      351
Arg Leu Leu Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp Gly Lys
75                80                85

cct cct gat atg aag aaa caa gag ctt gct aaa aga tac tca aaa aga      399
Pro Pro Asp Met Lys Lys Gln Glu Leu Ala Lys Arg Tyr Ser Lys Arg
90                95                100                105

gat gat gca acc aaa gat ctg act gag gca gta gag gta gga gat aaa      447
Asp Asp Ala Thr Lys Asp Leu Thr Glu Ala Val Glu Val Gly Asp Lys

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gta gag gca cct tct gaa gca gaa gca gaa tgt gca gcc ctt tgc ata Val Glu Ala Pro Ser Glu Ala Glu Ala Glu Cys Ala Ala Leu Cys Ile 155 160 165	591
aac gat aag gtg ttc gct gtt gct tca gaa gat atg gac tcc ctt act Asn Asp Lys Val Phe Ala Val Ala Ser Glu Asp Met Asp Ser Leu Thr 170 175 180 185	639
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aaa ata cct gtg atg gaa ttt gat gtt gcc aag gtt ttg gag gag ctt Lys Ile Pro Val Met Glu Phe Asp Val Ala Lys Val Leu Glu Glu Leu 205 210 215	735
gaa ctc acc atg gac cag ttc att gat ttg tgc atc ctg tgt gga tgt Glu Leu Thr Met Asp Gln Phe Ile Asp Leu Cys Ile Leu Cys Gly Cys 220 225 230	783
gac tat tgt gat agc atc aaa ggt atc ggg ggg caa aca gct ctg aaa Asp Tyr Cys Asp Ser Ile Lys Gly Ile Gly Gln Thr Ala Leu Lys 235 240 245	831
ctt att cgt caa cat ggg tcc ata gaa agc atc ttg gag aat ctt aat Leu Ile Arg Gln His Gly Ser Ile Glu Ser Ile Leu Glu Asn Leu Asn 250 255 260 265	879
aaa gac aga tat caa att cct gag gac tgg cct tac caa gaa gct cga Lys Asp Arg Tyr Gln Ile Pro Glu Asp Trp Pro Tyr Gln Glu Ala Arg 270 275 280	927
cgc ttg ttc aag gag cct aat gtc aca ttg gat att cct gag cta aaa Arg Leu Phe Lys Glu Pro Asn Val Thr Leu Asp Ile Pro Glu Leu Lys 285 290 295	975
tgg act gca cct gat gag gag ggt ctc ata agt ttc ctg gta aaa gat Trp Thr Ala Pro Asp Glu Glu Gly Leu Ile Ser Phe Leu Val Lys Asp 300 305 310	1023
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tct gcc aag aat aaa tcg tcg caa gga aga ctc gag tcc ttt ttc aag Ser Ala Lys Asn Lys Ser Ser Gln Gly Arg Leu Glu Ser Phe Phe Lys 330 335 340 345	1119
cca act gcc acc aca tca gca cgg cta aaa cgg aag gag act tcg gat Pro Thr Ala Thr Ser Ala Pro Leu Lys Arg Lys Glu Thr Ser Asp 350 355 360	1167

Val Thr Lys Ala Ile Glu Lys Ile Lys Ser Ala Lys Asn Lys Ser Ser
325 330 335

Gln Gly Arg Leu Glu Ser Phe Phe Lys Pro Thr Ala Thr Thr Ser Ala
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15 20 25

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Gly Arg Lys Ile Ala Val Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu

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Ile Val Val Gly Arg Thr Gly Met Glu Thr Leu Thr Asn Glu Ala Gly

45 50 55

gaa gtc act agt cat ttg caa gga atg ttc aac cgg aca ata aga tta 303

Glu Val Thr Ser His Leu Gln Gly Met Phe Asn Arg Thr Ile Arg Leu

60 65 70 75

ctg gaa gcg gga atc aag cca gtt tat gtt ttt gat ggc aag cct cct 351

Leu Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp Gly Lys Pro Pro

80 85 90

gat atg aag aaa caa gag ctt gct aaa aga tac tca aaa aga gat gat 399

Asp Met Lys Lys Gln Glu Leu Ala Lys Arg Tyr Ser Lys Arg Asp Asp

95 100 105

gca acc aaa gat ctg act gag gca gta gag gta gga gat aaa gat gcg 447

Ala Thr Lys Lys Asp Leu Thr Glu Ala Val Glu Val Gly Asp Lys Asp Ala

110 115 120

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Ile Glu Lys Leu Ser Lys Arg Thr Val Lys Val Thr Arg Gln His Asn

125 130 135

gaa gat tgt aaa cgg cta tta aga ctt atg ggg gtt cct gtt gta gag 543

Glu Asp Cys Lys Arg Leu Leu Arg Leu Met Gly Val Pro Val Val Glu

140 145 150 155

gca cct tct gaa gca gaa gca gaa tgt gca gcc ctt tgc ata aac gat 591

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Lys	Val	Phe	Ala	Val	Ala	Ser	Glu	Asp	Met	Asp	Ser	Leu	Thr	Phe	Gly		
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Pro	Val	Met	Glu	Phe	Asp	Val	Ala	Lys	Val	Leu	Glu	Glu	Leu	Glu	Leu		
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Lys	Asn	Lys	Ser	Ser	Gln	Gly	Arg	Leu	Glu	Ser	Phe	Phe	Lys	Pro	Thr		
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 35 40 45
 Thr Gly Met Glu Thr Leu Thr Asn Glu Ala Gly Glu Val Thr Ser His
 50 55 60
 Leu Gln Gly Met Phe Asn Arg Thr Ile Arg Leu Leu Glu Ala Gly Ile
 65 70 75 80
 Lys Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Asp Met Lys Lys Gln
 85 90 95
 Glu Leu Ala Lys Arg Tyr Ser Lys Arg Asp Asp Ala Thr Lys Asp Leu
 100 105 110
 Thr Glu Ala Val Glu Val Gly Asp Lys Asp Ala Ile Glu Lys Leu Ser
 115 120 125
 Lys Arg Thr Val Lys Val Thr Arg Gln His Asn Glu Asp Cys Lys Arg
 130 135 140
 Leu Leu Arg Leu Met Gly Val Pro Val Val Glu Ala Pro Ser Glu Ala
 145 150 155 160
 Glu Ala Glu Cys Ala Ala Leu Cys Ile Asn Asp Lys Val Phe Ala Val
 165 170 175
 Ala Ser Glu Asp Met Asp Ser Leu Thr Phe Gly Ala Pro Arg Phe Leu
 180 185 190
 Arg His Leu Met Asp Pro Ser Ser Lys Lys Ile Pro Val Met Glu Phe
 195 200 205
 Asp Val Ala Lys Val Leu Glu Glu Leu Glu Thr Met Asp Gln Phe
 210 215 220
 Ile Asp Leu Cys Ile Leu Cys Gly Cys Asp Tyr Cys Asp Ser Ile Lys
 225 230 235 240
 Gly Ile Gly Gly Gln Thr Ala Leu Lys Leu Ile Arg Gln His Gly Ser
 245 250 255
 Ile Glu Ser Ile Leu Glu Asn Leu Asn Lys Asp Arg Tyr Gln Ile Pro
 260 265 270
 Glu Asp Trp Pro Tyr Gln Glu Ala Arg Arg Leu Phe Lys Glu Pro Asn
 275 280 285
 Val Thr Leu Asp Ile Pro Glu Leu Lys Trp Thr Ala Pro Asp Glu Glu
 290 295 300
 Gly Leu Ile Ser Phe Leu Val Lys Asp Asn Gly Phe Asn Glu Asp Arg
 305 310 315 320
 Val Arg Lys Ala Ile Glu Lys Ile Lys Ser Ala Lys Asn Lys Ser Ser
 325 330 335
 Gln Gly Arg Leu Glu Ser Phe Phe Lys Pro Thr Ala Thr Thr Ser Ala
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<210> 5
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operator	name	signature	category	code	comment
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\mathbf{B}	base	float	scalar	$\text{base}(\text{float})$	base of a triangle
\mathbf{C}	center	float	scalar	$\text{center}(\text{float})$	center of a circle
\mathbf{D}	diameter	float	scalar	$\text{diameter}(\text{float})$	diameter of a circle
\mathbf{E}	edge	float	scalar	$\text{edge}(\text{float})$	edge of a square
\mathbf{F}	face	float	scalar	$\text{face}(\text{float})$	face of a cube
\mathbf{G}	gap	float	scalar	$\text{gap}(\text{float})$	gap between two objects
\mathbf{H}	height	float	scalar	$\text{height}(\text{float})$	height of a triangle
\mathbf{I}	in	float	scalar	$\text{in}(\text{float})$	in a set
\mathbf{J}	join	float	scalar	$\text{join}(\text{float})$	join of two objects
\mathbf{K}	key	float	scalar	$\text{key}(\text{float})$	key of a lock
\mathbf{L}	length	float	scalar	$\text{length}(\text{float})$	length of a line
\mathbf{M}	max	float	scalar	$\text{max}(\text{float})$	maximum value
\mathbf{N}	min	float	scalar	$\text{min}(\text{float})$	minimum value
\mathbf{O}	object	float	scalar	$\text{object}(\text{float})$	object of a class
\mathbf{P}	parent	float	scalar	$\text{parent}(\text{float})$	parent of a child
\mathbf{Q}	quantity	float	scalar	$\text{quantity}(\text{float})$	quantity of an item
\mathbf{R}	radius	float	scalar	$\text{radius}(\text{float})$	radius of a circle
\mathbf{S}	side	float	scalar	$\text{side}(\text{float})$	side of a square
\mathbf{T}	time	float	scalar	$\text{time}(\text{float})$	time of an event
\mathbf{U}	unit	float	scalar	$\text{unit}(\text{float})$	unit of measurement
\mathbf{V}	value	float	scalar	$\text{value}(\text{float})$	value of a variable
\mathbf{W}	width	float	scalar	$\text{width}(\text{float})$	width of a rectangle
\mathbf{X}	x	float	scalar	$\text{x}(\text{float})$	x-coordinate of a point
\mathbf{Y}	y	float	scalar	$\text{y}(\text{float})$	y-coordinate of a point
\mathbf{Z}	z	float	scalar	$\text{z}(\text{float})$	z-coordinate of a point
\mathbf{A}^*	area*	float	scalar	$\text{area}^*(\text{float})$	area of a square*
\mathbf{B}^*	base*	float	scalar	$\text{base}^*(\text{float})$	base of a triangle*
\mathbf{C}^*	center*	float	scalar	$\text{center}^*(\text{float})$	center of a circle*
\mathbf{D}^*	diameter*	float	scalar	$\text{diameter}^*(\text{float})$	diameter of a circle*
\mathbf{E}^*	edge*	float	scalar	$\text{edge}^*(\text{float})$	edge of a square*
\mathbf{F}^*	face*	float	scalar	$\text{face}^*(\text{float})$	face of a cube*
\mathbf{G}^*	gap*	float	scalar	$\text{gap}^*(\text{float})$	gap between two objects*
\mathbf{H}^*	height*	float	scalar	$\text{height}^*(\text{float})$	height of a triangle*
\mathbf{I}^*	in*	float	scalar	$\text{in}^*(\text{float})$	in a set*
\mathbf{J}^*	join*	float	scalar	$\text{join}^*(\text{float})$	join of two objects*
\mathbf{K}^*	key*	float	scalar	$\text{key}^*(\text{float})$	key of a lock*
\mathbf{L}^*	length*	float	scalar	$\text{length}^*(\text{float})$	length of a line*
\mathbf{M}^*	max*	float	scalar	$\text{max}^*(\text{float})$	maximum value*
\mathbf{N}^*	min*	float	scalar	$\text{min}^*(\text{float})$	minimum value*
\mathbf{O}^*	object*	float	scalar	$\text{object}^*(\text{float})$	object of a class*
\mathbf{P}^*	parent*	float	scalar	$\text{parent}^*(\text{float})$	parent of a child*
\mathbf{Q}^*	quantity*	float	scalar	$\text{quantity}^*(\text{float})$	quantity of an item*
\mathbf{R}^*	radius*	float	scalar	$\text{radius}^*(\text{float})$	radius of a circle*
\mathbf{S}^*	side*	float	scalar	$\text{side}^*(\text{float})$	side of a square*
\mathbf{T}^*	time*	float	scalar	$\text{time}^*(\text{float})$	time of an event*
\mathbf{U}^*	unit*	float	scalar	$\text{unit}^*(\text{float})$	unit of measurement*
\mathbf{V}^*	value*	float	scalar	$\text{value}^*(\text{float})$	value of a variable*
\mathbf{W}^*	width*	float	scalar	$\text{width}^*(\text{float})$	width of a rectangle*
\mathbf{X}^*	x*	float	scalar	$\text{x}^*(\text{float})$	x-coordinate of a point*
\mathbf{Y}^*	y*	float	scalar	$\text{y}^*(\text{float})$	y-coordinate of a point*
\mathbf{Z}^*					

operator	\hat{H}	\hat{H}_0	\hat{H}_1	\hat{H}_2	\hat{H}_3	\hat{H}_4	\hat{H}_5	\hat{H}_6	\hat{H}_7	\hat{H}_8	\hat{H}_9	\hat{H}_{10}	\hat{H}_{11}	\hat{H}_{12}	\hat{H}_{13}	\hat{H}_{14}	\hat{H}_{15}	\hat{H}_{16}	\hat{H}_{17}	\hat{H}_{18}	\hat{H}_{19}	\hat{H}_{20}	\hat{H}_{21}	\hat{H}_{22}	\hat{H}_{23}	\hat{H}_{24}	\hat{H}_{25}	\hat{H}_{26}	\hat{H}_{27}	\hat{H}_{28}	\hat{H}_{29}	\hat{H}_{30}	\hat{H}_{31}	\hat{H}_{32}	\hat{H}_{33}	\hat{H}_{34}	\hat{H}_{35}	\hat{H}_{36}	\hat{H}_{37}	\hat{H}_{38}	\hat{H}_{39}	\hat{H}_{40}	\hat{H}_{41}	\hat{H}_{42}	\hat{H}_{43}	\hat{H}_{44}	\hat{H}_{45}	\hat{H}_{46}	\hat{H}_{47}	\hat{H}_{48}	\hat{H}_{49}	\hat{H}_{50}	\hat{H}_{51}	\hat{H}_{52}	\hat{H}_{53}	\hat{H}_{54}	\hat{H}_{55}	\hat{H}_{56}	\hat{H}_{57}	\hat{H}_{58}	\hat{H}_{59}	\hat{H}_{60}	\hat{H}_{61}	\hat{H}_{62}	\hat{H}_{63}	\hat{H}_{64}	\hat{H}_{65}	\hat{H}_{66}	\hat{H}_{67}	\hat{H}_{68}	\hat{H}_{69}	\hat{H}_{70}	\hat{H}_{71}	\hat{H}_{72}	\hat{H}_{73}	\hat{H}_{74}	\hat{H}_{75}	\hat{H}_{76}	\hat{H}_{77}	\hat{H}_{78}	\hat{H}_{79}	\hat{H}_{80}	\hat{H}_{81}	\hat{H}_{82}	\hat{H}_{83}	\hat{H}_{84}	\hat{H}_{85}	\hat{H}_{86}	\hat{H}_{87}	\hat{H}_{88}	\hat{H}_{89}	\hat{H}_{90}	\hat{H}_{91}	\hat{H}_{92}	\hat{H}_{93}	\hat{H}_{94}	\hat{H}_{95}	\hat{H}_{96}	\hat{H}_{97}	\hat{H}_{98}	\hat{H}_{99}
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gta aaa gat aat ggt ttc aac gaa gat cgg gtg aca aag gcc ata gag Val Lys Asp Asn Gly Phe Asn Glu Asp Arg Val Thr Lys Ala Ile Glu 315 320 325	1014
aag atc aaa tct gcc aag aat aaa tcg tcg caa gga aga ctc gag tcc Lys Ile Lys Ser Ala Lys Asn Lys Ser Ser Gln Gly Arg Leu Glu Ser 330 335 340	1062
ttt ttc aag cca act gcc acc aca tca gca cgg cta aaa cgg aag gag Phe Phe Lys Pro Thr Ala Thr Thr Ser Ala Pro Leu Lys Arg Lys Glu 345 350 355	1110
act tcg gat aaa aca agc aag gca gct gcg aac aag aaa aca aag gct Thr Ser Asp Lys Thr Ser Lys Ala Ala Ala Asn Lys Lys Thr Lys Ala 360 365 370	1158
ggt gga aag aag aaa taatcttgga tgcttgatgt acaactacga ctacgaaagc Gly Gly Lys Lys Lys 375	1213
agcgggtggcg tgatcacttc gcttagatta tttaactccc tgttttaact cagagctttg gtaaaagtgc gcccatgttt caagctgggg taagttagtt gtgtttgaag agattggtgt accaagtaac aaaacttato gctgtttttt gaataaaaaa aaaaaaaa	1273 1333 1381

<210> 6

<211> 379

<212> PRT

<213> Zea mays

<400> 6

Met Gly Ile Lys Gly Leu Thr Lys Leu Leu Ala Asp Asn Ala Pro Lys 1 5 10 15
Ala Met Lys Glu Gln Lys Phe Glu Ser Tyr Phe Gly Arg Lys Ile Ala 20 25 30
Val Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Val Val Gly Arg 35 40 45
Thr Gly Met Glu Thr Leu Thr Asn Glu Ala Gly Glu Val Thr Ser His 50 55 60

Leu Gln Gly Met Phe Asn Arg Thr Ile Arg Leu Leu Glu Ala Gly Ile
 65 70 75 80
 Lys Pro Val Tyr Val Phe Asp Gly Lys Pro Asp Met Lys Lys Gln
 85 90 95
 Glu Leu Ala Lys Arg Tyr Ser Lys Arg Asp Ala Thr Lys Asp Leu
 100 105 110
 Thr Glu Ala Val Glu Val Gly Asp Lys Asp Ala Ile Glu Lys Leu Ser
 115 120 125
 Lys Arg Thr Val Lys Val Thr Arg Gln His Asn Glu Asp Cys Lys Arg
 130 135 140
 Leu Leu Arg Leu Met Gly Val Pro Val Val Glu Ala Pro Ser Glu Ala
 145 150 155 160
 Glu Ala Glu Cys Ala Ala Leu Cys Ile Asn Asp Lys Val Phe Ala Val
 165 170 175
 Ala Ser Glu Asp Met Asp Ser Leu Thr Phe Gly Ala Pro Arg Phe Leu
 180 185 190
 Arg His Leu Met Asp Pro Ser Ser Lys Lys Ile Pro Val Met Glu Phe
 195 200 205
 Asp Val Ala Lys Val Leu Glu Glu Leu Glu Thr Met Asp Gln Phe
 210 215 220
 Ile Asp Leu Cys Ile Leu Cys Gly Cys Asp Tyr Cys Asp Ser Ile Lys
 225 230 235 240
 Gly Ile Gly Gly Gln Thr Ala Leu Lys Leu Ile Arg Gln His Gly Ser
 245 250 255
 Ile Glu Ser Ile Leu Glu Asn Leu Asn Lys Asp Arg Tyr Gln Ile Pro
 260 265 270
 Glu Asp Trp Pro Tyr Gln Glu Ala Arg Arg Leu Phe Lys Glu Pro Asn
 275 280 285
 Val Thr Leu Asp Ile Pro Glu Leu Lys Trp Thr Ala Pro Asp Glu Glu
 290 295 300
 Gly Thr Ile Ser Phe Leu Val Lys Asp Asn Gly Phe Asn Glu Asp Arg
 305 310 315 320
 Val Thr Lys Ala Ile Glu Lys Ile Lys Ser Ala Lys Asn Lys Ser Ser
 325 330 335
 Gln Gly Arg Leu Glu Ser Phe Phe Lys Pro Thr Ala Thr Thr Ser Ala
 340 345 350
 Pro Leu Lys Arg Lys Glu Thr Ser Asp Lys Thr Ser Lys Ala Ala Ala
 355 360 365
 Asn Lys Lys Thr Lys Ala Gly Gly Lys Lys Lys
 370 375

<210> 7
 <211> 1478
 <212> DNA
 <213> Zea mays
 <220>
 <221> CDS
 <222> (97)...(1233)

<400> 7
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 cgcgccgc caccggccac agcgccgca gacgag atg ggc atc aag ggt ttg 114
 Met Gly Ile Lys Gly Leu
 1 5
 acg aaa ctg ctg gcg gac aat gcg ccc aag gcg atg aag gag cag aag 162
 Thr Lys Leu Leu Ala Asp Asn Ala Pro Lys Ala Met Lys Glu Gln Lys
 10 15 20
 ttc gag agc tac ttc ggc cgc aaa atc gcc gtc gag gcc agc atg agc 210

gaa gct cga cgc ttg ttc aag gag cct aat gtc act ttg gat att cct 978
 Glu Ala Arg Arg Leu Phe Lys Glu Pro Asn Val Thr Leu Asp Ile Pro
 280 285 290

gag cta aaa tgg act gca cct gat gag gag ggt ctc ata agt ttc ctg 1026
 Glu Leu Lys Trp Thr Ala Pro Asp Glu Gly Leu Ile Ser Phe Leu
 295 300 305 310

gta aaa gat aat ggt ttc aat gaa gat cgg gtg aca aag gcc ata gag 1074
 Val Lys Asp Asn Gly Phe Asn Glu Asp Arg Val Thr Lys Ala Ile Glu
 315 320 325

aag atc aaa tct gcc aag aat aaa tcg tcg caa gga aga ctc gag tcc 1122
 Lys Ile Lys Ser Ala Lys Asn Lys Ser Ser Gln Gly Arg Leu Glu Ser
 330 335 340

ttt ttc aag cca act gcc acc aca tca gca cgg cta aaa cgg aag gag 1170
 Phe Phe Lys Pro Thr Ala Thr Thr Ser Ala Pro Leu Lys Arg Lys Glu
 345 350 355

act tcg gat aaa aca agc aag gca gct gcg aac aag aaa aca aag gct 1218
 Thr Ser Asp Lys Thr Ser Lys Ala Ala Asn Lys Lys Thr Lys Ala
 360 365 370

ggt gga aag aag aaa taatcttgga tgcttgatgt acaactacga ctacgaaagc 1273
 Gly Gly Lys Lys Lys
 375

agcgggtggca tgatcacttc gcctagatta ttttaactccc tggttttaact cagacotttg 1333
 gtgaaagttt gcccatgttt caagctgggg taagtttagtt gtggttggaag agattgggtg 1393
 accaagtaac aaaacttctc gctgtttttt acttcttgct ctttgaagta tgtatgcagc 1453
 taaaaaaaaa aaaaaaaaaa aaaaa 1478

<210> 8
 <211> 379
 <212> PRT
 <213> Zea mays

<400> 8
 Met Gly Ile Lys Gly Leu Thr Lys Leu Leu Ala Asp Asn Ala Pro Lys
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 Ala Met Lys Glu Gln Lys Phe Glu Ser Tyr Phe Gly Arg Lys Ile Ala
 20 25 30
 Val Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Val Val Gly Arg
 35 40 45
 Thr Gly Met Glu Thr Leu Thr Asn Glu Ala Gly Glu Val Thr Ser His
 50 55 60
 Leu Gln Gly Met Phe Asn Arg Thr Ile Arg Leu Glu Ala Gly Ile
 65 70 75 80
 Lys Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Asp Met Lys Lys Gln
 85 90 95
 Glu Leu Ala Lys Arg Tyr Ser Lys Arg Asp Asp Ala Thr Lys Asp Leu
 100 105 110
 Thr Glu Ala Val Glu Val Gly Asp Lys Asp Ala Ile Glu Lys Leu Ser
 115 120 125
 Lys Arg Thr Val Lys Val Thr Arg Gln His Asn Glu Asp Cys Lys Arg
 130 135 140
 Leu Leu Arg Leu Met Gly Val Pro Val Val Glu Ala Pro Ser Glu Ala
 145 150 155 160

Glu Ala Glu Cys Ala Ala Leu Cys Ile Asn Asp Lys Val Phe Ala Val
 165 170 175
 Ala Ser Glu Asp Lys Asp Ser Leu Thr Phe Gly Ala Pro Arg Phe Leu
 180 185 190
 Arg His Leu Met Asp Pro Ser Ser Lys Ile Pro Val Met Glu Phe
 195 200 205
 Asp Val Ala Lys Val Leu Glu Glu Leu Thr Met Asp Gln Phe
 210 215 220
 Ile Asp Leu Cys Ile Leu Cys Gly Cys Asp Tyr Cys Asp Ser Ile Lys
 225 230 235 240
 Gly Ile Gly Gly Gln Thr Ala Leu Lys Leu Ile Arg Gln His Gly Ser
 245 250 255
 Ile Glu Ser Ile Leu Glu Asn Leu Asn Lys Asp Arg Tyr Gln Ile Pro
 260 265 270
 Glu Asp Trp Pro Tyr Gln Glu Ala Arg Arg Leu Phe Lys Glu Pro Asn
 275 280 285
 Val Thr Leu Asp Ile Pro Glu Leu Lys Trp Thr Ala Pro Asp Glu Glu
 290 295 300
 Gly Leu Ile Ser Phe Leu Val Lys Asp Asn Gly Phe Asn Glu Asp Arg
 305 310 315 320
 Val Thr Lys Ala Ile Glu Lys Ile Lys Ser Ala Lys Asn Lys Ser Ser
 325 330 335
 Gln Gly Arg Leu Glu Ser Phe Phe Lys Pro Thr Ala Thr Thr Ser Ala
 340 345 350
 Pro Leu Lys Arg Lys Glu Thr Ser Asp Lys Thr Ser Lys Ala Ala Ala
 355 360 365
 Asn Lys Lys Thr Lys Ala Gly Gly Lys Lys Lys
 370 375

<210> 9
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide based upon an adaptor
 used for cDNA library construction and poly(dT) to
 remove clones which have a poly(A) tail but no
 cDNA insert.

<400> 9
 tcgacccacg cgctccgaaaa aaaaaaaaaa aaaaaa
 36

<210> 10
 <211> 380
 <212> PRT
 <213> Homo sapiens

<400> 10
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 1 5 10 15
 Ala Ile Arg Glu Asn Asp Ile Lys Ser Tyr Phe Gly Arg Lys Val Ala
 20 25 30
 Ile Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Ala Val Arg Gln
 35 40 45
 Gly Gly Asp Val Leu Gln Asn Glu Glu Gly Glu Thr Thr Ser His Leu
 50 55 60
 Met Gly Met Phe Tyr Arg Thr Ile Arg Met Met Glu Asn Gly Ile Lys
 65 70 75 80

Pro	Val	Tyr	Val	Phe	Asp	Gly	Lys	Pro	Pro	Gln	Leu	Lys	Ser	Gly	Glu
				85					90					95	
Leu	Ala	Lys	Arg	Ser	Glu	Arg	Arg	Ala	Glu	Ala	Glu	Lys	Gln	Leu	Gln
			100					105					110		
Gln	Ala	Gln	Ala	Ala	Gly	Ala	Glu	Gln	Glu	Val	Glu	Lys	Phe	Thr	Lys
			115				120						125		
Arg	Leu	Val	Lys	Val	Thr	Lys	Gln	His	Asn	Asp	Glu	Cys	Lys	His	Leu
	130					135					140				
Leu	Ser	Leu	Met	Gly	Ile	Pro	Tyr	Leu	Asp	Ala	Pro	Ser	Glu	Ala	Glu
	145				150					155					160
Ala	Ser	Cys	Ala	Ala	Leu	Val	Lys	Ala	Gly	Lys	Val	Tyr	Ala	Ala	Ala
			165						170					175	
Thr	Glu	Asp	Met	Asp	Cys	Leu	Thr	Phe	Gly	Ser	Pro	Val	Leu	Met	Arg
			180						185				190		
His	Leu	Thr	Ala	Ser	Glu	Ala	Lys	Lys	Leu	Pro	Ile	Gln	Glu	Phe	His
		195					200					205			
Leu	Ser	Arg	Ile	Leu	Gln	Glu	Leu	Gly	Leu	Asn	Gln	Glu	Gln	Phe	Val
		210				215					220				
Asp	Leu	Cys	Ile	Leu	Leu	Gly	Ser	Asp	Tyr	Cys	Glu	Ser	Ile	Arg	Gly
	225				230					235					240
Ile	Gly	Pro	Lys	Arg	Ala	Val	Asp	Leu	Ile	Gln	Lys	His	Lys	Ser	Ile
			245						250						255
Glu	Glu	Ile	Val	Arg	Arg	Leu	Asp	Pro	Asn	Lys	Tyr	Pro	Val	Pro	Glu
			260					265					270		
Asn	Trp	Leu	His	Lys	Glu	Ala	His	Gln	Leu	Phe	Leu	Glu	Pro	Glu	Val
		275					280						285		
Leu	Asp	Pro	Glu	Ser	Val	Glu	Leu	Lys	Trp	Ser	Glu	Pro	Asn	Glu	Glu
		290				295					300				
Glu	Leu	Ile	Lys	Phe	Met	Cys	Gly	Glu	Lys	Gln	Phe	Ser	Glu	Glu	Arg
	305				310					315					320
Ile	Arg	Ser	Gly	Val	Lys	Arg	Leu	Ser	Lys	Ser	Arg	Gln	Gly	Ser	Thr
			325						330					335	
Gln	Gly	Arg	Leu	Asp	Asp	Phe	Phe	Lys	Val	Thr	Gly	Ser	Leu	Ser	Ser
			340					345					350		
Ala	Lys	Arg	Lys	Glu	Pro	Glu	Pro	Lys	Gly	Ser	Thr	Lys	Lys	Lys	Ala
		355					360						365		
Lys	Thr	Gly	Ala	Ala	Gly	Lys	Phe	Lys	Arg	Gly	Lys				
	370					375					380				